In the Claims

Please amend the claims as shown below.

1. (Currently Amended) A method of ~~identifying~~ determining a nucleotide sequence of a nucleic acid comprising:

loading a first short sequencing reaction product at a first loading time into one or more lanes of ~~a~~ an electrophoresis sequencing ~~gel~~ device;

loading a second short sequencing reaction product onto the same one or more lanes of the sequencing ~~gel~~ device as the first short sequencing reaction product at a second loading time, wherein the first loading time and the second loading time are sufficiently temporally separated to separate the first short sequencing reaction product from the second short sequencing reaction product by electrophoresis; and

~~performing gel or capillary electrophoresis on~~ determining the sequence of the first short sequencing reaction product and ~~on~~ the sequence of the second short sequencing reaction product.

2. (Currently Amended) The method of claim 1, wherein the first short sequencing reaction product is produced from a region comprising a SNP (single nucleotide polymorphism).

3. (Currently Amended) The method of claim 1, wherein the first short sequencing reaction product is produced from an EST (expressed sequence tag).

4. (Previously Presented) The method of claim 1, wherein the first short sequencing reaction product and second short sequencing reaction product are each about 20 bases or shorter.

5. (Previously Presented) The method of claim 1, wherein the first short sequencing reaction product is a run off sequencing reaction product.

6. (Currently Amended) A method of determining the nucleotide sequence of a portion of a nucleic acid comprising:

a) isolating the nucleic acid from a nucleic acid library wherein the library comprises a recognition site of an enzyme that cuts at least 1 base downstream of the recognition site, wherein the recognition site is positioned within 1 base of an insert of the library;

b) amplifying the nucleic acid;

c) digesting the amplified nucleic acid with the enzyme;

d) performing a run-off sequencing reaction utilizing a primer that hybridizes to a region of an amplified fragment of said amplified and digested nucleic acid at or upstream of the recognition site to form a first sequencing reaction product;

e) loading a first sequencing reaction product at a first loading time into one or more lanes of an electrophoresis sequencing device; and

f) ~~performing electrophoresis analysis on~~ determining the sequence of the first sequencing reaction product.

7. (Currently Amended) The method of claim 6, further comprising the steps of:

g) loading a second sequencing reaction product onto the same one or more lanes of the ~~an~~ electrophoresis sequencing device as the first sequencing reaction product at a second loading time, wherein the first loading time and the second loading time are sufficiently temporally separated to separate the first sequencing reaction product from the second sequencing reaction product by electrophoresis; and

h) ~~and performing electrophoresis analysis on~~ determining the sequence of the second sequencing reaction product.

8. (Previously Presented) The method of claim 6, wherein the enzyme is a restriction enzyme.

9. (Currently Amended) The method of claim 8, wherein the restriction enzyme is ~~BpmI~~ BpmI

10. (Currently Amended)The method of claim 6, wherein the ~~electrophoresis performed is~~ sequence is determined using gel electrophoresis.

11. (Currently Amended) The method of claim 6, wherein the ~~electrophoresis is performed with~~ sequence is determined using a capillary apparatus.

12. (Canceled)

13. (Canceled)

14. (Currently Amended) A method of determining the nucleotide sequence of a portion of a nucleic acid comprising:

a) isolating the nucleic acid from a nucleic acid library wherein the library comprises a recognition site of an enzyme that cuts at least 1 base downstream of the recognition site, wherein the recognition site is positioned within 1 base of an insert of the library;

b) amplifying the nucleic acid;

c) digesting the amplified nucleic acid with the enzyme;

d) performing a run-off sequencing reaction utilizing a primer that hybridizes to a region of ~~the~~ an amplified fragment of said amplified and digested nucleic acid at or upstream of the recognition site to form a ~~first~~ sequencing reaction product;

e) ~~performing mass spectrophotometry on of the first~~ determining the sequence of the sequencing reaction product, wherein the sequence is determined using mass spectrophotometry.